Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:28:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240058.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6240058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:28:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,214,657
Mapped reads	1,812,212 / 81.83%
Unmapped reads	402,445 / 18.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,191 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	137,237 / 6.2%
Duplication rate	5.73%
Clipped reads	1,246,070 / 56.26%

2.2. ACGT Content

Number/percentage of A's	28,429,587 / 25.76%
Number/percentage of C's	19,604,641 / 17.76%
Number/percentage of T's	34,661,710 / 31.41%
Number/percentage of G's	27,602,053 / 25.01%
Number/percentage of N's	69,443 / 0.06%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.3797

2.4. Mapping Quality

Mean Mapping Quality	40.4

2.5. Mismatches and indels

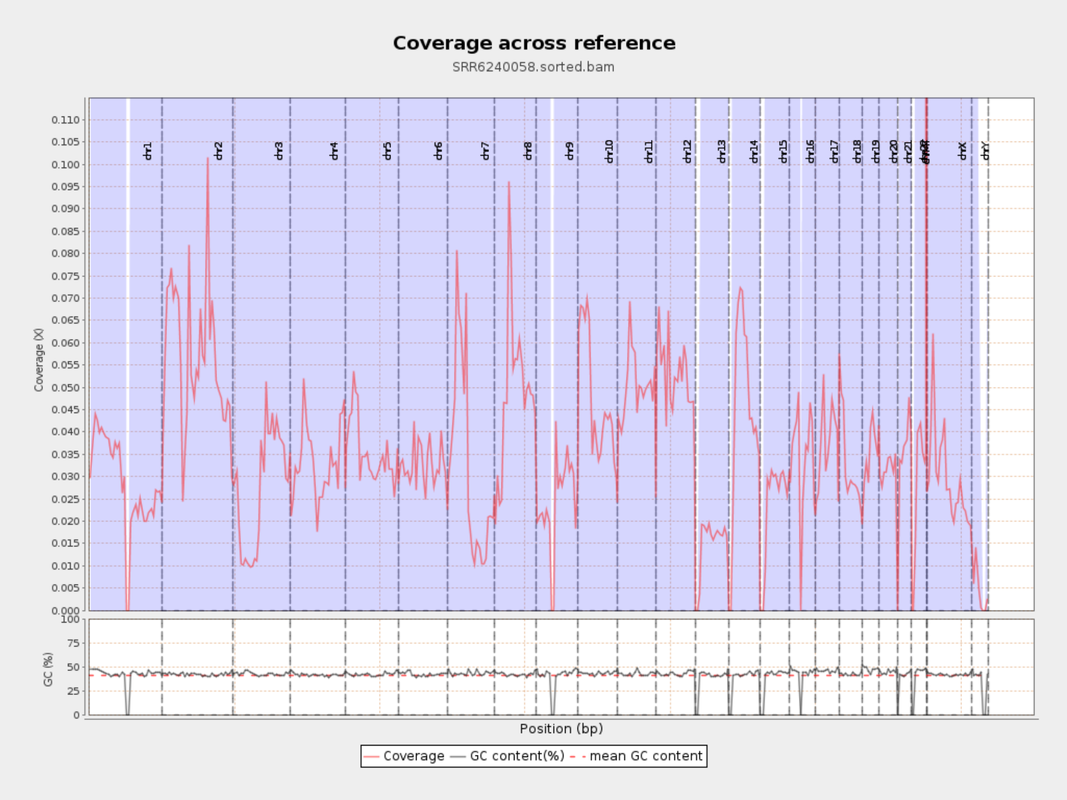
General error rate	1%
Mismatches	1,086,054
Insertions	8,114
Mapped reads with at least one insertion	0.44%
Deletions	35,480
Mapped reads with at least one deletion	1.94%
Homopolymer indels	47.22%

2.6. Chromosome stats

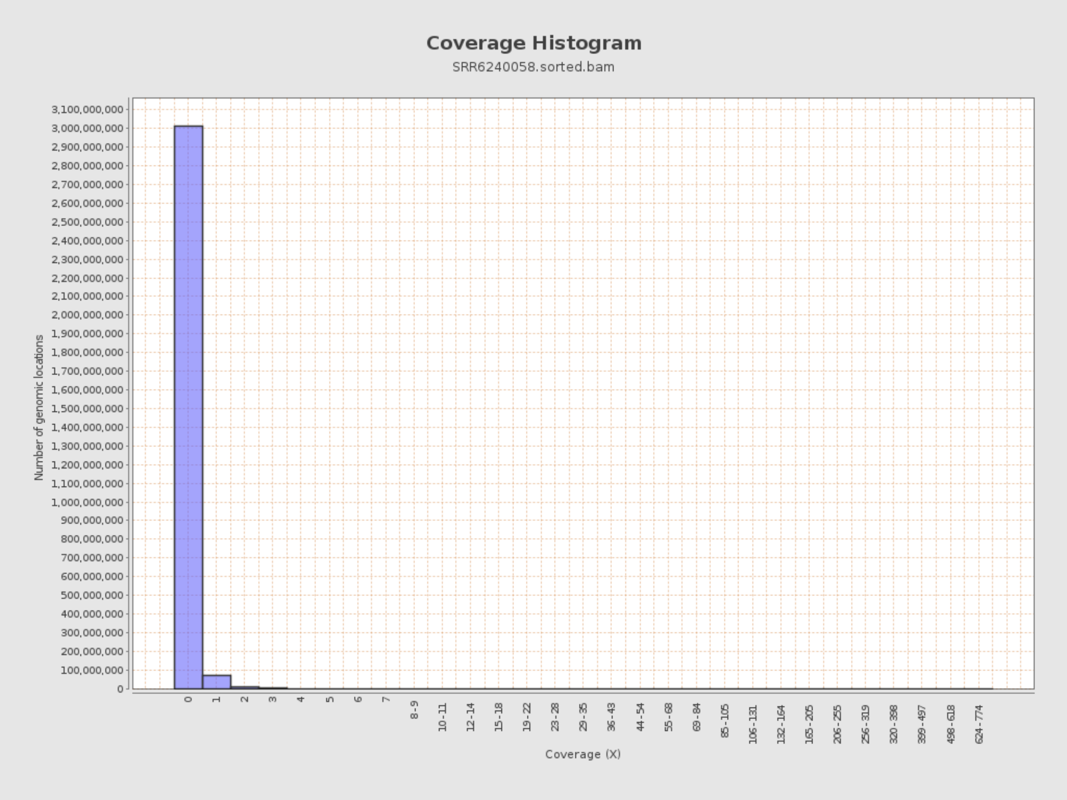
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7099401	0.0285	0.3522
chr2	243199373	13864570	0.057	0.5795
chr3	198022430	5397619	0.0273	0.2121
chr4	191154276	6339920	0.0332	0.2712
chr5	180915260	6442426	0.0356	0.2459
chr6	171115067	5581704	0.0326	0.295
chr7	159138663	5089820	0.032	0.7175

chr8	146364022	7207541	0.0492	0.4132
chr9	141213431	3413985	0.0242	0.3726
chr10	135534747	6517853	0.0481	0.3544
chr11	135006516	6739285	0.0499	0.5552
chr12	133851895	7097501	0.053	0.3013
chr13	115169878	1694993	0.0147	0.1519
chr14	107349540	4873653	0.0454	0.2862
chr15	102531392	2427070	0.0237	0.2899
chr16	90354753	3083547	0.0341	0.2593
chr17	81195210	3037815	0.0374	0.3183
chr18	78077248	2565280	0.0329	0.5587
chr19	59128983	2081708	0.0352	0.3379
chr20	63025520	1965896	0.0312	0.2348
chr21	48129895	1662439	0.0345	0.2552
chr22	51304566	1350189	0.0263	0.2053
chrMT	16571	20643	1.2457	1.7319
chrX	155270560	4593469	0.0296	0.2804
chrY	59373566	280501	0.0047	0.1079

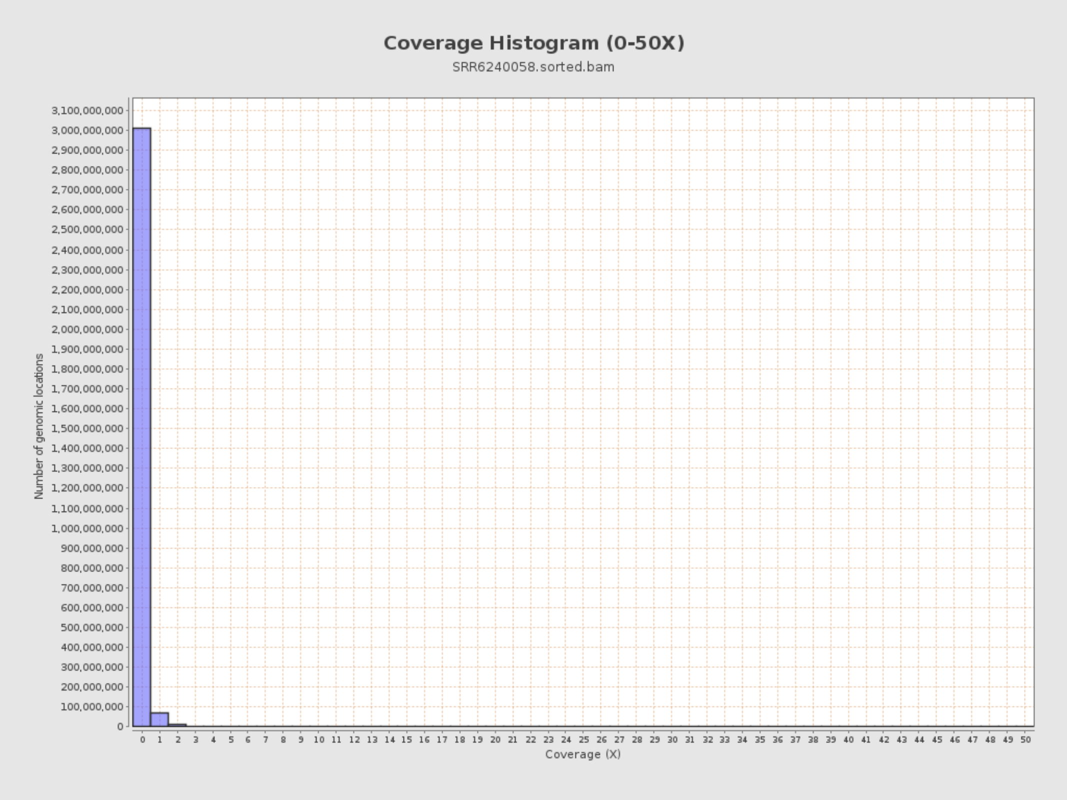
3. Results : Coverage across reference



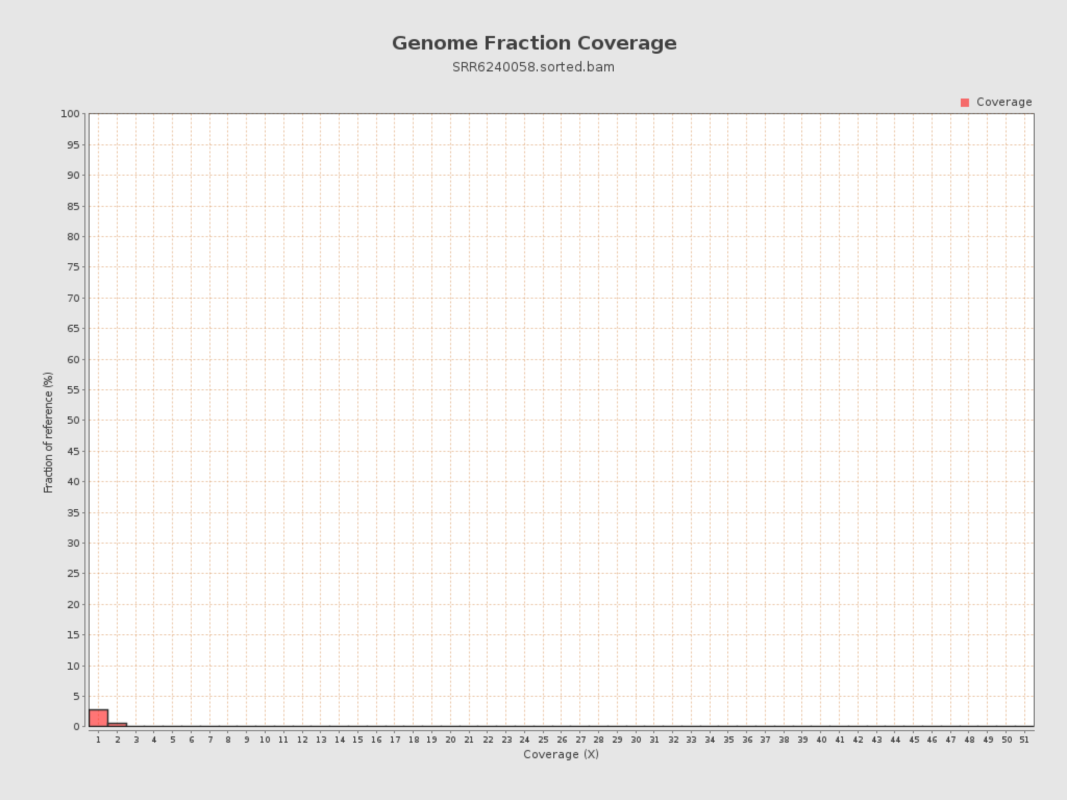
4. Results : Coverage Histogram



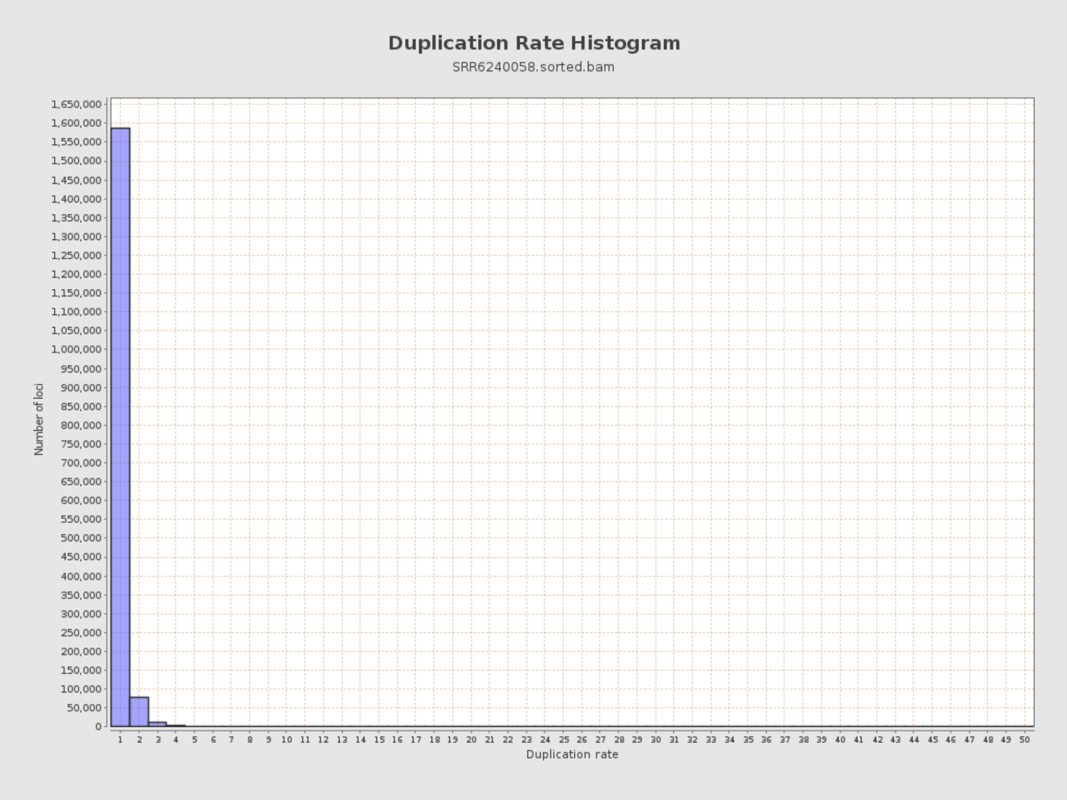
5. Results : Coverage Histogram (0-50X)



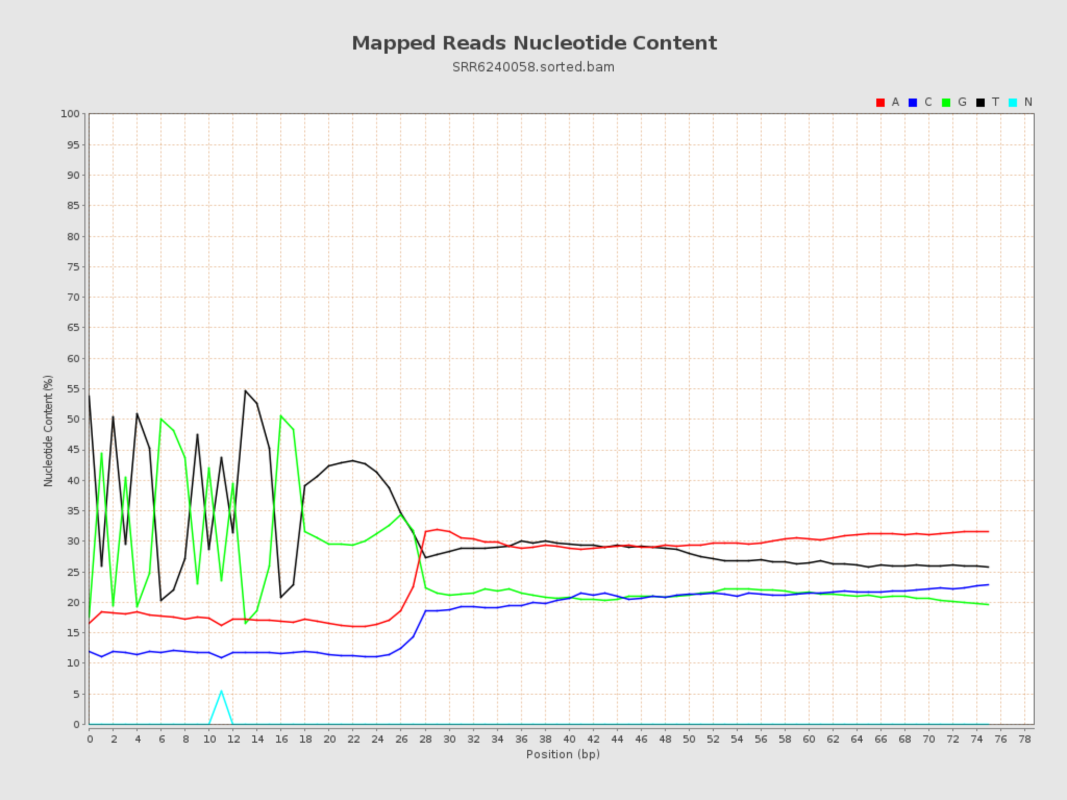
6. Results : Genome Fraction Coverage



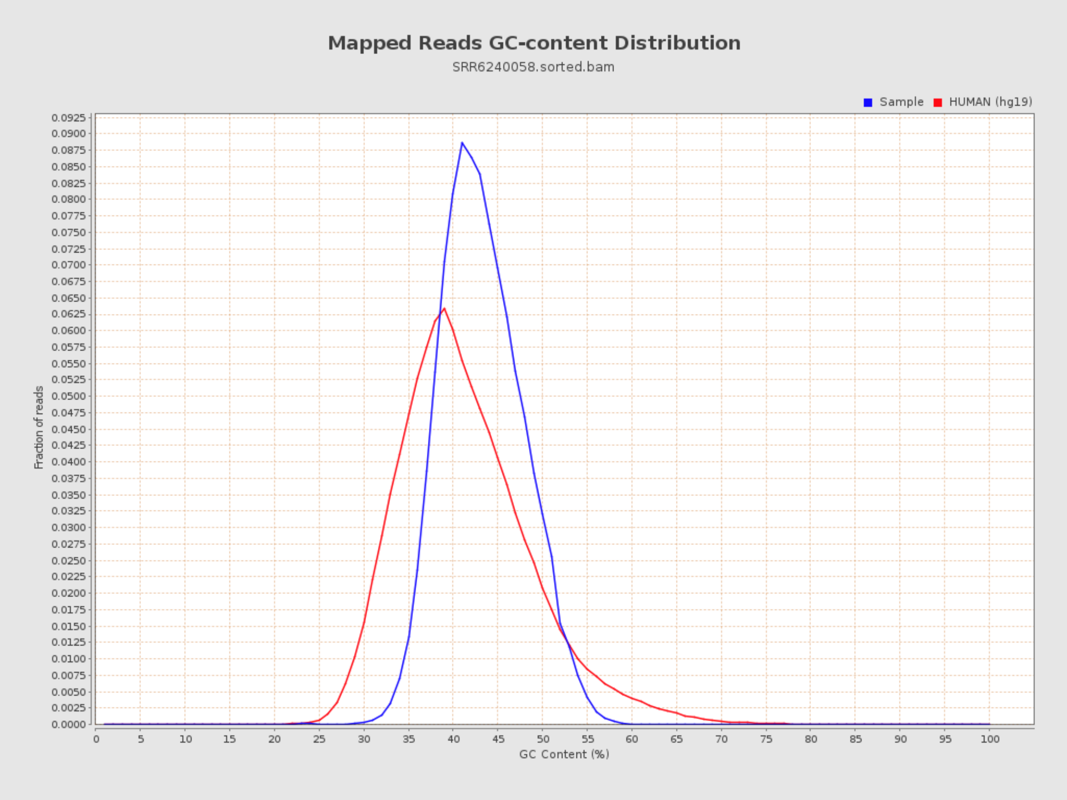
7. Results : Duplication Rate Histogram



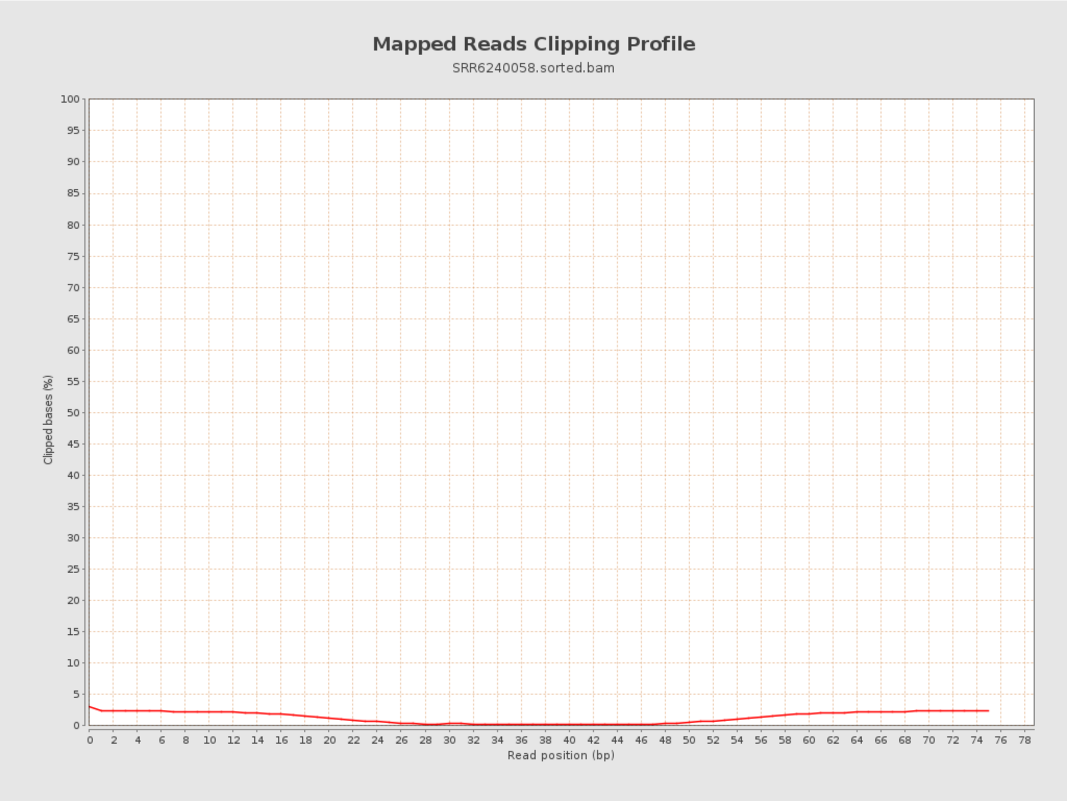
8. Results : Mapped Reads Nucleotide Content



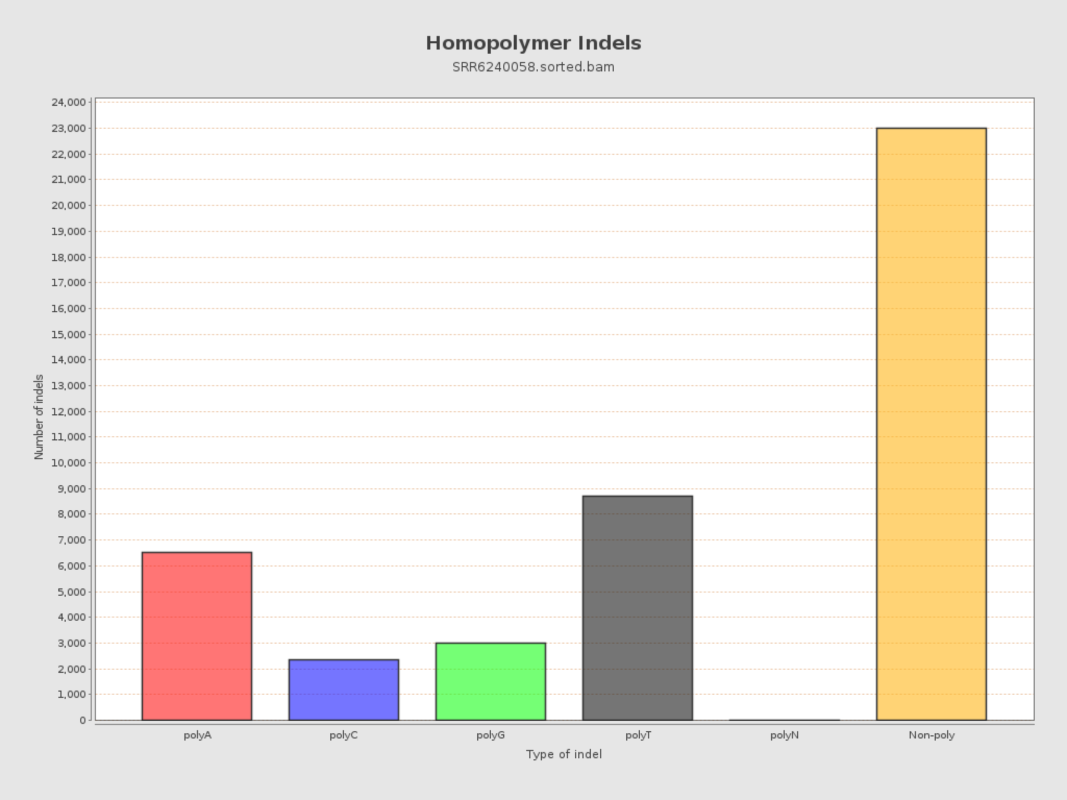
9. Results : Mapped Reads GC-content Distribution



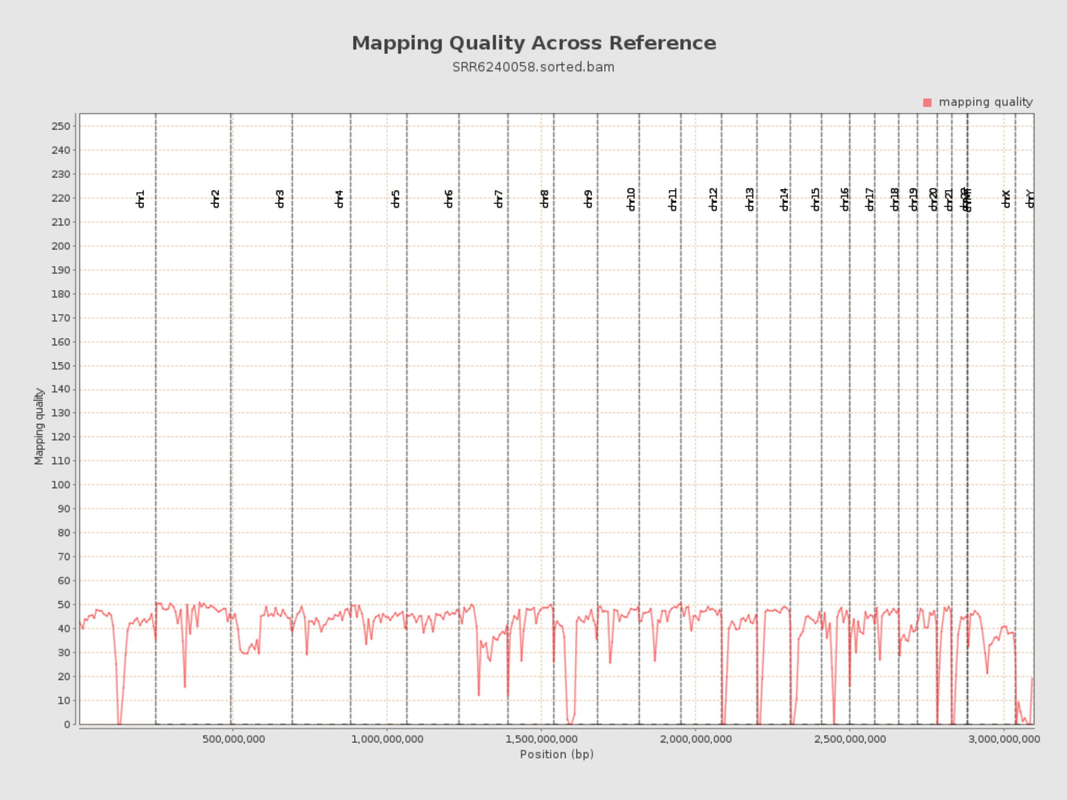
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram